

RAW SEQUENCE LISTING

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Application Serial Number: 10/518, 414
Source: PCT
Date Processed by STIC: 11/03/2005

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/518,414

DATE: 11/03/2005
TIME: 08:22:19

Input Set : A:\Seq 1st P1031.ST25.txt
Output Set: N:\CRF4\11032005\J518414.raw

3 <110> APPLICANT: Chr. Hansen A/S
4 Maarten van den Brink, Johannes
5 Harboe, Marianne K
6 Petersen, Steen Guldager
7 Rahbek-Nielsen, Henrik
9 <120> TITLE OF INVENTION: IMPROVED METHOD OF PRODUCING AN ASPARTIC PROTEASE
POLYPEPTIDE IN
10 A RECOMBINANT HOST ORGANISM
12 <130> FILE REFERENCE: P1031US00
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/518,414
C--> 14 <141> CURRENT FILING DATE: 2004-12-17
14 <150> PRIOR APPLICATION NUMBER: PA 2002 0092
15 <151> PRIOR FILING DATE: 2002-06-17
17 <160> NUMBER OF SEQ ID NOS: 8
19 <170> SOFTWARE: PatentIn version 3.3
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 323
23 <212> TYPE: PRT
24 <213> ORGANISM: Bos taurus
26 <400> SEQUENCE: 1
28 Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp Ser Gln Tyr
29 1 5 10 15
32 Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe Thr Val Leu
33 20 25 30
36 Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile Tyr Cys Lys
37 35 40 45
40 Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg Lys Ser Ser
41 50 55 60
44 Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr Gly Thr Gly
45 65 70 75 80
48 Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val Ser Asn Ile
49 85 90 95
52 Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu Pro Gly Asp
53 100 105 110
56 Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met Ala Tyr Pro
57 115 120 125
60 Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn Met Met Asn
61 130 135 140
64 Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met Asp Arg Asn
65 145 150 155 160
68 Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro Ser Tyr Tyr
69 165 170 175
72 Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln Tyr Trp Gln
73 180 185 190

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76 Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val Ala Cys Glu
77 195 200 205
80 Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys Leu Val Gly
81 210 215 220
84 Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly Ala Thr Gln
85 225 230 235 240
88 Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu Ser Tyr Met
89 245 250 255
92 Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro Leu Thr Pro
93 260 265 270
96 Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser Gly Phe Gln
97 275 280 285
100 Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val Phe Ile Arg
101 290 295 300
104 Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val Gly Leu Ala
105 305 310 315 320
108 Lys Ala Ile
112 <210> SEQ ID NO: 2
113 <211> LENGTH: 1142
114 <212> TYPE: DNA
115 <213> ORGANISM: artificial
117 <220> FEATURE:
118 <223> OTHER INFORMATION: DNA fragment comprising a DNA fragment of 1138 bp designed
to
119 comprise a N-H-T glycosylation site and unique SalI and XhoI
120 sites for cloning purposes (modB-XS).
122 <400> SEQUENCE: 2
123 cggtcgaccg ctacggtgac tgacacctgg cgtgccgaga tcactcgat cccctctac 60
125 aaggcaagt ctctcgtaa ggctctcaag gagcacggtc tgctcgagga ttctctgcag 120
127 aagcagcagt acggcatcg ctctaagtac agcgggttcg gcgaggtggc cagcgtgcct 180
129 ctcactaact acctggacag ccagttacttc ggtaagatct accttggcac tccccctcag 240
131 gagttcaccc ttctgttca tactggttcc agcgacttct ggttccctc catctactgt 300
133 aagagcaacg cttgaagaa ccaccagcgc ttcgatcctc gcaagtccag cacttccag 360
135 aaccttggca agccctttc catccactac ggtactggca gcatgcaggg tattcttggc 420
137 tacgacaccc ttaccgtgtc caacatcgatc gatattcagc agaccgtggg tctgagcacc 480
139 caggagcctg gcgatgtctt cacttacgatc gagttcgatg gtatcctcgg catggcttac 540
141 ccctccctgg cctctgagta ctctatccct gtgttcgaca acatgatgaa ccggcaccc 600
143 gtcgctcagg atctgttca gctgtacatg gaccgttaacg gtcaggagtc catgttact 660
145 ctgggcgcca tcgatccctc ttactacacc gttccctcc actgggttcc tgtgaccgtc 720
147 cagcagttact ggcagttcac cgtggacagc gtcactatct cggcgtgg tggcttgc 780
149 gaggggtggct gtcaggccat cttgtatact ggtaccagca agctcgccgg cccctccaggc 840
151 gacatcctga acatccagca ggctatcggt gccacccaga accagtaacgg cgagttcgat 900
153 atcgactgcg ataaccttcc ttacatcgatc actgtggtt tcgagatcaa cggtaaatgt 960
155 tacccttta ctcctctgc ttacacttcc caggatcagg gttctgtac ctctggttc 1020
157 cagtctgaga accacagcca gaagtggatc cttggcgatg tcttcatccg cgagtactac 1080
159 tccgtttcg accgtgccaa caacctgggt ggtctcgatc aggccatctg atcccttaga 1140
161 gt 1142
164 <210> SEQ ID NO: 3
165 <211> LENGTH: 408
166 <212> TYPE: DNA

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167 <213> ORGANISM: artificial
 169 <220> FEATURE:
 170 <223> OTHER INFORMATION: an approximately 410 bp SalI-SphII I fragment made using
 171 synthetic oligonucleotides (SEQ ID XXX-1)
 173 <400> SEQUENCE: 3
 174 cggtcgaccg ctacgggtgac tgacacacctgg cgtggcggaga tcactcgcat cccctctac 60
 176 aaggcaagt ctctcgtaa ggctctcaag gagcacggtc tgctcgagga tttctgcag 120
 178 aagcagcagt acggcatcg ctctaagttac agcggttcg gcgagggtgc cagcgtgcct 180
 180 ctcactaact acctggacag ccagtacttc ggtaagatct accttggcac tccccctcag 240
 182 gagttcaccc ttctgttgcg tactggttcc agcgacttct gggttccctc catctactgt 300
 184 aagagcaacg cttgcaagaa ccaccaggcgc ttcgatccctc gcaagtccag caccctccag 360
 186 aacccggca agcccttccatccactac ggtactggca gcatgcag 408
 189 <210> SEQ ID NO: 4
 190 <211> LENGTH: 233
 191 <212> TYPE: DNA
 192 <213> ORGANISM: artificial
 194 <220> FEATURE:
 195 <223> OTHER INFORMATION: an approximately 220 bp SphI-BsrGI fragment made using
 synthetic
 196 oligonucleotides (SEQ ID XXX-2)
 198 <400> SEQUENCE: 4
 199 gcagcatgca gggatccctt ggctacgaca ccgttaccgt gtccaaacatc gtcgatattc 60
 201 agcagaccgt gggatcgagc acccaggagc ctggcgatgt cttcaatc gccgagttcg 120
 203 atggatccctt cggcatggct tacccttccc tggctctga gtactctatc cctgtgttcg 180
 205 acaacatgtatc gaaaccggcac ctctgtcgatc aggtatgtt cagcgtgtac atg 233
 208 <210> SEQ ID NO: 5
 209 <211> LENGTH: 200
 210 <212> TYPE: DNA
 211 <213> ORGANISM: Artificial
 213 <220> FEATURE:
 214 <223> OTHER INFORMATION: an approximately 190 bp BsrGI-KpnI fragment made using
 synthetic
 215 oligonucleotides (SEQ ID XXX-3)
 217 <400> SEQUENCE: 5
 218 gctgtacat ggaccgtaac ggtcaggagt ccatgtttac tctggcgcc atcgatccct 60
 220 cttaatcacac cggatccctc cactgggttc ctgtgaccgt ccagcgtac tggcagttca 120
 222 cctgtggacag cgtcactatc tccggcgatgg ttgtggcttg cgagggtggc tgtcaggcca 180
 224 tccttgcatac tggtaccatc 200
 227 <210> SEQ ID NO: 6
 228 <211> LENGTH: 334
 229 <212> TYPE: DNA
 230 <213> ORGANISM: artificial
 232 <220> FEATURE:
 233 <223> OTHER INFORMATION: an approximately 320 bp KpnI-XbaI fragment made using
 synthetic
 234 oligonucleotides (SEQ ID XXX-4)
 236 <400> SEQUENCE: 6
 237 ctgggtaccatc caagctcgatc ggcccttccatc ggcgacatctt gaaatccatc caggctatcg 60
 239 gtcgcacccaa gaaccgtac ggcgagttcg atatcgactg cgataacccatc tcttacatgc 120
 241 ctactgtgtt tttcgatc aacggtaaga tgtacccct tactccatct gcttacactt 180
 243 cccaggatca gggatcccttgc accttgcgtt tccagtctga gaaaccacagc cagaagtgaa 240
 245 tccttgcatac tggatccatc cgcgatctt actccgtatc cgaccgtgcc aacaacctgg 300

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247 tgggtctcgc taaggccatc tgatcctcta gagt 334
 250 <210> SEQ ID NO: 7
 251 <211> LENGTH: 334
 252 <212> TYPE: DNA
 253 <213> ORGANISM: artificial
 255 <220> FEATURE:
 256 <223> OTHER INFORMATION: a modified KpnI-XbaI fragment designed for construction of
 the
 257 modBM gene (SEQ ID XXX-5).
 259 <400> SEQUENCE: 7
 260 ctggtaccag caagctcgcc ggcccccctcca gcgcacatcctt gaacatccag caggctatcg 60
 262 gtgccaccca gaaccaggatc ggcgagttcg atatcgactg cgataacacctt tcttacatgc 120
 264 ctactgtggt tttcgagatc aacggtaaga tgtacccctt tactccttctt gcttacactt 180
 266 cccaggatca gggctctgtt acctctggtt tccagtctga gaaccacacc cagaagtgg 240
 268 tccttggcga tgtcttcatc cgcgagttactt actccgtctt cgaccgtgcc aacaacctgg 300
 270 tgggtctcgc taaggccatc tgatcctcta gagt 334
 273 <210> SEQ ID NO: 8
 274 <211> LENGTH: 66
 275 <212> TYPE: DNA
 276 <213> ORGANISM: artificial
 278 <220> FEATURE:
 279 <223> OTHER INFORMATION: synthetic polylinker (SalI-SphI-BsrGI-KpnI-XbaI) (SEQ ID
 XXX-6)
 281 <400> SEQUENCE: 8
 282 ggccaggcgc gccttccatg gaagaatgcg gccgctaaac catcgatggc tcgagttggc 60
 284 gcgcca 66

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/03/2005
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:2,3,4,5,6,7,8

VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date